

DT05 Rec'd PCT/PTO 18 OCT 2004

&lt;110&gt; Lynkeus Biotech GmbH

<120> Means and Methods for the Specific Modulation of Target Genes in the  
CNS and the Eye and Methods for Their Identification

&lt;130&gt; LY01A04/P-WO

&lt;150&gt; EP02008761.5

&lt;151&gt; 2002-04-18

&lt;150&gt; US 60/431,173

&lt;151&gt; 2002-12-05

&lt;160&gt; 10

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 2500

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (25)..(2097)

&lt;223&gt; Homo sapiens cyclic nucleotide gated channel alpha 1

```
<400> 1
tatattactt aaacaaccaa agat atg aaa cta tcc atg aag aac aat att      51
                        Met Lys Leu Ser Met Lys Asn Asn Ile
                        1                      5

atc aat aca cag cag tct ttt gta acc atg ccc aat gtg att gta cca      99
Ile Asn Thr Gln Gln Ser Phe Val Thr Met Pro Asn Val Ile Val Pro
10                      15                      20                      25
```

gat att gaa aag gaa ata cga agg atg gaa aat gga gca tgc agc tcc Asp Ile Glu Lys Glu Ile Arg Arg Met Glu Asn Gly Ala Cys Ser Ser 30 35 40	147
ttt tct gag gat gat gac agt gcc tat aca tct gaa gaa tca gag aat Phe Ser Glu Asp Asp Asp Ser Ala Tyr Thr Ser Glu Glu Ser Glu Asn 45 50 55	195
gaa aac cct cat gca agg ggt tcc ttt agt tat aag tca ctc aga aag Glu Asn Pro His Ala Arg Gly Ser Phe Ser Tyr Lys Ser Leu Arg Lys 60 65 70	243
gga gga cca tca cag agg gag cag tac ctg cct ggt gcc att gcc att Gly Gly Pro Ser Gln Arg Glu Gln Tyr Leu Pro Gly Ala Ile Ala Ile 75 80 85	291
ttt aat gtg aac aac agc agc aat aag gac cag gaa cca gag gaa aaa Phe Asn Val Asn Asn Ser Ser Asn Lys Asp Gln Glu Pro Glu Glu Lys 90 95 100 105	339
aag aaa aag aaa aaa gaa aag aag agc aag tca gat gat aaa aac gaa Lys Lys Lys Lys Lys Glu Lys Lys Ser Lys Ser Asp Asp Lys Asn Glu 110 115 120	387
aat aaa aac gac cca gag aag aaa aag aag aaa aag gac aaa gag aag Asn Lys Asn Asp Pro Glu Lys Lys Lys Lys Lys Lys Asp Lys Glu Lys 125 130 135	435
aaa aag aaa gag gag aaa agc aaa gat aag aaa gaa cac cac aag aaa Lys Lys Lys Glu Glu Lys Ser Lys Asp Lys Lys Glu His His Lys Lys 140 145 150	483
gaa gtt gtg gtt att gat ccc tcg gga aac aca tat tac aac tgg ctg Glu Val Val Val Ile Asp Pro Ser Gly Asn Thr Tyr Tyr Asn Trp Leu 155 160 165	531
ttt tgc atc aca tta cct gtt atg tac aac tgg aca atg gtt att gcc Phe Cys Ile Thr Leu Pro Val Met Tyr Asn Trp Thr Met Val Ile Ala 170 175 180 185	579
aga gca tgt ttt gat gaa ctt caa tct gat tac cta gaa tat tgg ctc Arg Ala Cys Phe Asp Glu Leu Gln Ser Asp Tyr Leu Glu Tyr Trp Leu 190 195 200	627
att ttg gat tac gta tca gac ata gtc tat tta atc gat atg ttt gta Ile Leu Asp Tyr Val Ser Asp Ile Val Tyr Leu Ile Asp Met Phe Val 205 210 215	675
cga aca agg aca ggt tac cta gaa caa gga ctg ctg gta aag gaa gaa Arg Thr Arg Thr Gly Tyr Leu Glu Gln Gly Leu Leu Val Lys Glu Glu 220 225 230	723
ctt aaa ctc ata aat aaa tat aaa tcc aac ttg caa ttt aaa ctt gat Leu Lys Leu Ile Asn Lys Tyr Lys Ser Asn Leu Gln Phe Lys Leu Asp 235 240 245	771
gtt ctg tca ctg ata cca act gat ttg ctg tat ttt aag tta ggg tgg Val Leu Ser Leu Ile Pro Thr Asp Leu Leu Tyr Phe Lys Leu Gly Trp 250 255 260 265	819
aac tat cca gaa att aga tta aac agg ttg tta cgg ttc tct cgt atg Asn Tyr Pro Glu Ile Arg Leu Asn Arg Leu Leu Arg Phe Ser Arg Met 270 275 280	867

ttt gag ttc ttc cag aga aca gaa aca agg aca aac tat cca aac atc	915
Phe Glu Phe Phe Gln Arg Thr Glu Thr Arg Thr Asn Tyr Pro Asn Ile	
285 290 295	
ttc agg att tcc aac ctt gtt atg tat atc gtc atc att atc cac tgg	963
Phe Arg Ile Ser Asn Leu Val Met Tyr Ile Val Ile Ile Ile His Trp	
300 305 310	
aat gca tgt gtg ttc tac tct att tct aaa gct att gga ttt gga aat	1011
Asn Ala Cys Val Phe Tyr Ser Ile Ser Lys Ala Ile Gly Phe Gly Asn	
315 320 325	
gat aca tgg gtc tac cct gat att aat gat cct gaa ttt ggc cgt ttg	1059
Asp Thr Trp Val Tyr Pro Asp Ile Asn Asp Pro Glu Phe Gly Arg Leu	
330 335 340 345	
gct aga aaa tac gta tac agc ctt tac tgg tct aca ctg act ttg act	1107
Ala Arg Lys Tyr Val Tyr Ser Leu Tyr Trp Ser Thr Leu Thr Leu Thr	
350 355 360	
acc att ggt gaa aca ccc cct ccc gtg agg gat tct gag tat gtc ttt	1155
Thr Ile Gly Glu Thr Pro Pro Pro Val Arg Asp Ser Glu Tyr Val Phe	
365 370 375	
gtg gtg gtt gat ttc cta att gga gtg tta att ttt gct acc atc gtt	1203
Val Val Val Asp Phe Leu Ile Gly Val Leu Ile Phe Ala Thr Ile Val	
380 385 390	
ggt aac ata ggt tct atg att tcc aac atg aat gca gcc aga gca gaa	1251
Gly Asn Ile Gly Ser Met Ile Ser Asn Met Asn Ala Ala Arg Ala Glu	
395 400 405	
ttt caa gca aga att gat gct atc aag caa tat atg cat ttt cga aat	1299
Phe Gln Ala Arg Ile Asp Ala Ile Lys Gln Tyr Met His Phe Arg Asn	
410 415 420 425	
gta agc aaa gat atg gaa aag agg gtt att aaa tgg ttt gac tac ctg	1347
Val Ser Lys Asp Met Glu Lys Arg Val Ile Lys Trp Phe Asp Tyr Leu	
430 435 440	
tgg acc aac aaa aaa aca gtt gat gag aaa gaa gtc tta aag tat cta	1395
Trp Thr Asn Lys Lys Thr Val Asp Glu Lys Glu Val Leu Lys Tyr Leu	
445 450 455	
cct gat aaa cta aga gca gaa att gcc atc aac gtt cac tta gac aca	1443
Pro Asp Lys Leu Arg Ala Glu Ile Ala Ile Asn Val His Leu Asp Thr	
460 465 470	
tta aaa aag gta cgc att ttt gct gat tgt gaa gct ggt ctg ttg gtg	1491
Leu Lys Lys Val Arg Ile Phe Ala Asp Cys Glu Ala Gly Leu Leu Val	
475 480 485	
gag ttg gtc ttg aaa ttg caa ccc caa gtc tac agt cct gga gat tat	1539
Glu Leu Val Leu Lys Leu Gln Pro Gln Val Tyr Ser Pro Gly Asp Tyr	
490 495 500 505	
att tgc aag aaa ggg gat atc gga cga gag atg tac att atc aag gaa	1587
Ile Cys Lys Lys Gly Asp Ile Gly Arg Glu Met Tyr Ile Ile Lys Glu	
510 515 520	
ggc aaa ctc gct gtg gtg gca gat gat gga gtc act cag ttt gtg gta	1635
Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr Gln Phe Val Val	

525	530	535	
ttg agc gat ggc agc acc ttc ggt gag atc agc att ctt aac att aaa Leu Ser Asp Gly Ser Thr Phe Gly Glu Ile Ser Ile Leu Asn Ile Lys 540 545 550			1683
ggg agc aaa gct ggc aat cga aga acg gcc aat att aaa agt att ggc Gly Ser Lys Ala Gly Asn Arg Arg Thr Ala Asn Ile Lys Ser Ile Gly 555 560 565			1731
tac tca gac ctg ttc tgt ctc tca aaa gat gac ctc atg gaa gct cta Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu Met Glu Ala Leu 570 575 580 585			1779
act gag tac cca gat gcc aaa act atg cta gaa gaa aaa ggg aag caa Thr Glu Tyr Pro Asp Ala Lys Thr Met Leu Glu Glu Lys Gly Lys Gln 590 595 600			1827
att tta atg aaa gat ggt cta ctg gat cta aac att gca aat gct ggc Ile Leu Met Lys Asp Gly Leu Leu Asp Leu Asn Ile Ala Asn Ala Gly 605 610 615			1875
agt gat cct aaa gat ctt gaa gag aag gtt act cga atg gag ggg tca Ser Asp Pro Lys Asp Leu Glu Glu Lys Val Thr Arg Met Glu Gly Ser 620 625 630			1923
gta gac ctc ctg caa acc agg ttt gcc cga atc ttg gct gag tat gag Val Asp Leu Leu Gln Thr Arg Phe Ala Arg Ile Leu Ala Glu Tyr Glu 635 640 645			1971
tcc atg cag cag aaa ctg aaa caa aga tta acc aag gtt gag aaa ttt Ser Met Gln Gln Lys Leu Lys Gln Arg Leu Thr Lys Val Glu Lys Phe 650 655 660 665			2019
ctg aaa ccg ctt att gac aca gaa ttt tca agt att gag gga cct tgg Leu Lys Pro Leu Ile Asp Thr Glu Phe Ser Ser Ile Glu Gly Pro Trp 670 675 680			2067
agc gaa agt ggg ccc atc gac tct aca tag aaccgaaaag ctggtcatta Ser Glu Ser Gly Pro Ile Asp Ser Thr 685 690			2117
acagggacat gcctcatgat ccttttgatc ctatgactga catcaactaa aattttaaag			2177
aagaggaaga ctgagttggg aaatttttcc atgaggaaaa tgtgcttttg tgcaaggtag			2237
agccacacacc tctctgagag atactatgat taaaaaagct ttatatctgg gatttttcac			2297
aactgataat gtgcaaagat ataaactgat taacttggtca gtgtctgtat tttctgattt			2357
tttcacatac gctcatttta tgtaatatcc ttcataaaaa tgaataagta gccctcactt			2417
tcatgccatt tccattgttg agtgaagcgt atttgaagta actgagaatt accatgtaca			2477
tcatatttgg gataacattt tta			2500

&lt;210&gt; 2

&lt;211&gt; 690

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 2

Met Lys Leu Ser Met Lys Asn Asn Ile Ile Asn Thr Gln Gln Ser Phe  
 1 5 10 15

Val Thr Met Pro Asn Val Ile Val Pro Asp Ile Glu Lys Glu Ile Arg  
 20 25 30

Arg Met Glu Asn Gly Ala Cys Ser Ser Phe Ser Glu Asp Asp Asp Ser  
 35 40 45

Ala Tyr Thr Ser Glu Glu Ser Glu Asn Glu Asn Pro His Ala Arg Gly  
 50 55 60

Ser Phe Ser Tyr Lys Ser Leu Arg Lys Gly Gly Pro Ser Gln Arg Glu  
 65 70 75 80

Gln Tyr Leu Pro Gly Ala Ile Ala Ile Phe Asn Val Asn Asn Ser Ser  
 85 90 95

Asn Lys Asp Gln Glu Pro Glu Glu Lys Lys Lys Lys Lys Lys Glu Lys  
 100 105 110

Lys Ser Lys Ser Asp Asp Lys Asn Glu Asn Lys Asn Asp Pro Glu Lys  
 115 120 125

Lys Lys Lys Lys Lys Asp Lys Glu Lys Lys Lys Lys Glu Glu Lys Ser  
 130 135 140

Lys Asp Lys Lys Glu His His Lys Lys Glu Val Val Val Ile Asp Pro  
 145 150 155 160

Ser Gly Asn Thr Tyr Tyr Asn Trp Leu Phe Cys Ile Thr Leu Pro Val  
 165 170 175

Met Tyr Asn Trp Thr Met Val Ile Ala Arg Ala Cys Phe Asp Glu Leu  
 180 185 190

Gln Ser Asp Tyr Leu Glu Tyr Trp Leu Ile Leu Asp Tyr Val Ser Asp  
 195 200 205

Ile Val Tyr Leu Ile Asp Met Phe Val Arg Thr Arg Thr Gly Tyr Leu  
 210 215 220

Glu Gln Gly Leu Leu Val Lys Glu Glu Leu Lys Leu Ile Asn Lys Tyr

225

230

235

240

Lys Ser Asn Leu Gln Phe Lys Leu Asp Val Leu Ser Leu Ile Pro Thr  
 245 250 255

Asp Leu Leu Tyr Phe Lys Leu Gly Trp Asn Tyr Pro Glu Ile Arg Leu  
 260 265 270

Asn Arg Leu Leu Arg Phe Ser Arg Met Phe Glu Phe Phe Gln Arg Thr  
 275 280 285

Glu Thr Arg Thr Asn Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val  
 290 295 300

Met Tyr Ile Val Ile Ile Ile His Trp Asn Ala Cys Val Phe Tyr Ser  
 305 310 315 320

Ile Ser Lys Ala Ile Gly Phe Gly Asn Asp Thr Trp Val Tyr Pro Asp  
 325 330 335

Ile Asn Asp Pro Glu Phe Gly Arg Leu Ala Arg Lys Tyr Val Tyr Ser  
 340 345 350

Leu Tyr Trp Ser Thr Leu Thr Leu Thr Thr Ile Gly Glu Thr Pro Pro  
 355 360 365

Pro Val Arg Asp Ser Glu Tyr Val Phe Val Val Val Asp Phe Leu Ile  
 370 375 380

Gly Val Leu Ile Phe Ala Thr Ile Val Gly Asn Ile Gly Ser Met Ile  
 385 390 395 400

Ser Asn Met Asn Ala Ala Arg Ala Glu Phe Gln Ala Arg Ile Asp Ala  
 405 410 415

Ile Lys Gln Tyr Met His Phe Arg Asn Val Ser Lys Asp Met Glu Lys  
 420 425 430

Arg Val Ile Lys Trp Phe Asp Tyr Leu Trp Thr Asn Lys Lys Thr Val  
 435 440 445

Asp Glu Lys Glu Val Leu Lys Tyr Leu Pro Asp Lys Leu Arg Ala Glu  
 450 455 460

Ile Ala Ile Asn Val His Leu Asp Thr Leu Lys Lys Val Arg Ile Phe  
 465 470 475 480

Ala Asp Cys Glu Ala Gly Leu Leu Val Glu Leu Val Leu Lys Leu Gln  
485 490 495

Pro Gln Val Tyr Ser Pro Gly Asp Tyr Ile Cys Lys Lys Gly Asp Ile  
500 505 510

Gly Arg Glu Met Tyr Ile Ile Lys Glu Gly Lys Leu Ala Val Val Ala  
515 520 525

Asp Asp Gly Val Thr Gln Phe Val Val Leu Ser Asp Gly Ser Thr Phe  
530 535 540

Gly Glu Ile Ser Ile Leu Asn Ile Lys Gly Ser Lys Ala Gly Asn Arg  
545 550 555 560

Arg Thr Ala Asn Ile Lys Ser Ile Gly Tyr Ser Asp Leu Phe Cys Leu  
565 570 575

Ser Lys Asp Asp Leu Met Glu Ala Leu Thr Glu Tyr Pro Asp Ala Lys  
580 585 590

Thr Met Leu Glu Glu Lys Gly Lys Gln Ile Leu Met Lys Asp Gly Leu  
595 600 605

Leu Asp Leu Asn Ile Ala Asn Ala Gly Ser Asp Pro Lys Asp Leu Glu  
610 615 620

Glu Lys Val Thr Arg Met Glu Gly Ser Val Asp Leu Leu Gln Thr Arg  
625 630 635 640

Phe Ala Arg Ile Leu Ala Glu Tyr Glu Ser Met Gln Gln Lys Leu Lys  
645 650 655

Gln Arg Leu Thr Lys Val Glu Lys Phe Leu Lys Pro Leu Ile Asp Thr  
660 665 670

Glu Phe Ser Ser Ile Glu Gly Pro Trp Ser Glu Ser Gly Pro Ile Asp  
675 680 685

Ser Thr  
690

&lt;210&gt; 3

&lt;211&gt; 3231

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (22) .. (2586)

&lt;223&gt; Homo sapiens phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant)

&lt;400&gt; 3

ctccagggac aggcagccac c	atg agc ctc agt gag gag cag gcc cgg agc	51
	Met Ser Leu Ser Glu Glu Gln Ala Arg Ser	
	1 5 10	
ttt ctg gac cag aac ccc gat ttt gcc cgc cag tac ttt ggg aag aaa		99
Phe Leu Asp Gln Asn Pro Asp Phe Ala Arg Gln Tyr Phe Gly Lys Lys		
	15 20 25	
ctg agc cct gag aat gtt ggc cgc ggc tgc gag gac ggg tgc ccg ccg		147
Leu Ser Pro Glu Asn Val Gly Arg Gly Cys Glu Asp Gly Cys Pro Pro		
	30 35 40	
gac tgc gac agc ctc cgg gac ctc tgc cag gtg gag gag agc acg gcg		195
Asp Cys Asp Ser Leu Arg Asp Leu Cys Gln Val Glu Glu Ser Thr Ala		
	45 50 55	
ctg ctg gag ctg gtg cag gat atg cag gag agc atc aac atg gag cgc		243
Leu Leu Glu Leu Val Gln Asp Met Gln Glu Ser Ile Asn Met Glu Arg		
	60 65 70	
gtg gtc ttc aag gtc ctg cgg cgc ctc tgc acc ctc ctg cag gcc gac		291
Val Val Phe Lys Val Leu Arg Arg Leu Cys Thr Leu Leu Gln Ala Asp		
	75 80 85 90	
cgc tgc agc ctc ttc atg tac cgc cag cgc aac ggc gtg gcc gag ctg		339
Arg Cys Ser Leu Phe Met Tyr Arg Gln Arg Asn Gly Val Ala Glu Leu		
	95 100 105	
gcc acc agg ctt ttc agc gtg cag ccg gac agc gtc ctg gag gac tgc		387
Ala Thr Arg Leu Phe Ser Val Gln Pro Asp Ser Val Leu Glu Asp Cys		
	110 115 120	
ctg gtg ccc ccc gac tcc gag atc gtc ttc cca ctg gac atc ggg gtc		435
Leu Val Pro Pro Asp Ser Glu Ile Val Phe Pro Leu Asp Ile Gly Val		
	125 130 135	
gtg ggc cac gtg gct cag acc aaa aag atg gtg aac gtc gag gac gtg		483
Val Gly His Val Ala Gln Thr Lys Lys Met Val Asn Val Glu Asp Val		
	140 145 150	
gcc gag tgc cct cac ttc agc tca ttt gct gac gag ctc act gac tac		531
Ala Glu Cys Pro His Phe Ser Ser Phe Ala Asp Glu Leu Thr Asp Tyr		
	155 160 165 170	
aag aca aag aat atg ctg gcc aca ccc atc atg aat ggc aaa gac gtc		579
Lys Thr Lys Asn Met Leu Ala Thr Pro Ile Met Asn Gly Lys Asp Val		
	175 180 185	



gtg gcg gtg atc atg gca gtg aac aag ctc aac ggc cca ttc ttc acc	627
Val Ala Val Ile Met Ala Val Asn Lys Leu Asn Gly Pro Phe Phe Thr	
190 195 200	
agc gaa gac gaa gat gtg ttc ttg aag tac ctg aat ttt gcc acg ttg	675
Ser Glu Asp Glu Asp Val Phe Leu Lys Tyr Leu Asn Phe Ala Thr Leu	
205 210 215	
tac ctg aag atc tat cac ctg agc tac ctc cac aac tgc gag acg cgc	723
Tyr Leu Lys Ile Tyr His Leu Ser Tyr Leu His Asn Cys Glu Thr Arg	
220 225 230	
cgc ggc cag gtg ctg ctg tgg tgc gcc aac aag gtg ttt gag gag ctg	771
Arg Gly Gln Val Leu Leu Trp Ser Ala Asn Lys Val Phe Glu Glu Leu	
235 240 245 250	
acg gac atc gag agg cag ttc cac aag gcc ttc tac acg gtg cgg gcc	819
Thr Asp Ile Glu Arg Gln Phe His Lys Ala Phe Tyr Thr Val Arg Ala	
255 260 265	
tac ctc aac tgc gag cgg tac tcc gtg ggc ctc ctg gac atg acc aag	867
Tyr Leu Asn Cys Glu Arg Tyr Ser Val Gly Leu Leu Asp Met Thr Lys	
270 275 280	
gag aag gaa ttt ttt gac gtg tgg tct gtg ctg atg gga gag tcc cag	915
Glu Lys Glu Phe Phe Asp Val Trp Ser Val Leu Met Gly Glu Ser Gln	
285 290 295	
ccg tac tgc ggc cca cgc acg cct gat ggc cgg gaa att gtc ttc tac	963
Pro Tyr Ser Gly Pro Arg Thr Pro Asp Gly Arg Glu Ile Val Phe Tyr	
300 305 310	
aaa gtg atc gac tac atc ctc cac ggc aag gag gag atc aag gtc att	1011
Lys Val Ile Asp Tyr Ile Leu His Gly Lys Glu Glu Ile Lys Val Ile	
315 320 325 330	
ccc aca ccc tca gcc gat cac tgg gcc ctg gcc agc ggc ctt cca agc	1059
Pro Thr Pro Ser Ala Asp His Trp Ala Leu Ala Ser Gly Leu Pro Ser	
335 340 345	
tac gtg gca gaa agc ggc ttt att tgt aac atc atg aat gct tcc gct	1107
Tyr Val Ala Glu Ser Gly Phe Ile Cys Asn Ile Met Asn Ala Ser Ala	
350 355 360	
gac gaa atg ttc aaa ttt cag gaa ggg gcc ctg gac gac tcc ggg tgg	1155
Asp Glu Met Phe Lys Phe Gln Glu Gly Ala Leu Asp Asp Ser Gly Trp	
365 370 375	
ctc atc aag aat gtg ctg tcc atg ccc atc gtc aac aag aag gag gag	1203
Leu Ile Lys Asn Val Leu Ser Met Pro Ile Val Asn Lys Lys Glu Glu	
380 385 390	
att gtg gga gtc gcc aca ttt tac aac agg aaa gac ggg aag ccc ttt	1251
Ile Val Gly Val Ala Thr Phe Tyr Asn Arg Lys Asp Gly Lys Pro Phe	
395 400 405 410	
gac gaa cag gac gag gtt ctc atg gag tcc ctg aca cag ttc ctg ggc	1299
Asp Glu Gln Asp Glu Val Leu Met Glu Ser Leu Thr Gln Phe Leu Gly	
415 420 425	
tgg tca gtg atg aac acc gac acc tac gac aag atg aac aag ctg gag	1347
Trp Ser Val Met Asn Thr Asp Thr Tyr Asp Lys Met Asn Lys Leu Glu	
430 435 440	

aac cgc aag gac atc gca cag gac atg gtc ctt tac cac gtg aag tgc Asn Arg Lys Asp Ile Ala Gln Asp Met Val Leu Tyr His Val Lys Cys 445 450 455	1395
gac agg gac gag atc cag ctc atc ctg cca acc aga gcg cgc ctg ggg Asp Arg Asp Glu Ile Gln Leu Ile Leu Pro Thr Arg Ala Arg Leu Gly 460 465 470	1443
aag gag cct gct gac tgc gat gag gac gag ctg ggc gaa atc ctg aag Lys Glu Pro Ala Asp Cys Asp Glu Asp Glu Leu Gly Glu Ile Leu Lys 475 480 485 490	1491
gag gag ctg cca ggg ccc acc aca ttt gac atc tac gaa ttc cac ttc Glu Glu Leu Pro Gly Pro Thr Thr Phe Asp Ile Tyr Glu Phe His Phe 495 500 505	1539
tct gac ctg gag tgc acc gaa ctg gac ctg gtc aaa tgt ggc atc cag Ser Asp Leu Glu Cys Thr Glu Leu Asp Leu Val Lys Cys Gly Ile Gln 510 515 520	1587
atg tac tac gag ctg ggc gtg gtc cga aag ttc cag atc ccc cag gag Met Tyr Tyr Glu Leu Gly Val Val Arg Lys Phe Gln Ile Pro Gln Glu 525 530 535	1635
gtc ctg gtg cgg ttc ctg ttc tcc atc agc aaa ggg tac cgg aga atc Val Leu Val Arg Phe Leu Phe Ser Ile Ser Lys Gly Tyr Arg Arg Ile 540 545 550	1683
acc tac cac aac tgg cgc cac ggc ttc aac gtg gcc cag acg atg ttc Thr Tyr His Asn Trp Arg His Gly Phe Asn Val Ala Gln Thr Met Phe 555 560 565 570	1731
acg ctg ctc atg acc ggc aaa ctg aag agc tac tac acg gac ctg gag Thr Leu Leu Met Thr Gly Lys Leu Lys Ser Tyr Tyr Thr Asp Leu Glu 575 580 585	1779
gcc ttc gcc atg gtg aca gcc ggc ctg tgc cat gac atc gac cac cgc Ala Phe Ala Met Val Thr Ala Gly Leu Cys His Asp Ile Asp His Arg 590 595 600	1827
ggc acc aac aac ctg tac cag atg aag tcc cag aac ccc ttg gct aag Gly Thr Asn Asn Leu Tyr Gln Met Lys Ser Gln Asn Pro Leu Ala Lys 605 610 615	1875
ctc cac ggc tcc tcg att ttg gag cgg cac cac ctg gag ttt ggg aag Leu His Gly Ser Ser Ile Leu Glu Arg His His Leu Glu Phe Gly Lys 620 625 630	1923
ttc ctg ctc tcg gag gag acc ctg aac atc tac cag aac ctg aac cgg Phe Leu Leu Ser Glu Glu Thr Leu Asn Ile Tyr Gln Asn Leu Asn Arg 635 640 645 650	1971
cgg cag cac gag cac gtg atc cac ctg atg gac atc gcc atc atc gcc Arg Gln His Glu His Val Ile His Leu Met Asp Ile Ala Ile Ile Ala 655 660 665	2019
acg gac ctg gcc ctg tac ttc aag aag aga gcg atg ttt cag aag atc Thr Asp Leu Ala Leu Tyr Phe Lys Lys Arg Ala Met Phe Gln Lys Ile 670 675 680	2067
gtg gat gag tcc aag aac tac cag gac aag aag agc tgg gtg gag tac Val Asp Glu Ser Lys Asn Tyr Gln Asp Lys Lys Ser Trp Val Glu Tyr	2115

11/16

685	690	695	
ctg tcc ctg gag acg acc cgg aag gag atc gtc atg gcc atg atg atg Leu Ser Leu Glu Thr Thr Arg Lys Glu Ile Val Met Ala Met Met Met 700 705 710			2163
aca gcc tgc gac ctg tct gcc atc acc aag ccc tgg gaa gtc cag agc Thr Ala Cys Asp Leu Ser Ala Ile Thr Lys Pro Trp Glu Val Gln Ser 715 720 725 730			2211
aag gtc gca ctt ctc gtg gct gct gag ttc tgg gag caa ggt gac ttg Lys Val Ala Leu Leu Val Ala Ala Glu Phe Trp Glu Gln Gly Asp Leu 735 740 745			2259
gaa agg aca gtc ttg gat cag cag ccc att cct atg atg gac cgg aac Glu Arg Thr Val Leu Asp Gln Gln Pro Ile Pro Met Met Asp Arg Asn 750 755 760			2307
aag gcg gcc gag ctc ccc aag ctg caa gtg ggc ttc atc gac ttc gtg Lys Ala Ala Glu Leu Pro Lys Leu Gln Val Gly Phe Ile Asp Phe Val 765 770 775			2355
tgc aca ttc gtg tac aag gag ttc tct cgt ttc cac gaa gag atc ctg Cys Thr Phe Val Tyr Lys Glu Phe Ser Arg Phe His Glu Glu Ile Leu 780 785 790			2403
ccc atg ttc gac cga ctg cag aac aat agg aaa gag tgg aag gcg ctg Pro Met Phe Asp Arg Leu Gln Asn Asn Arg Lys Glu Trp Lys Ala Leu 795 800 805 810			2451
gct gat gag tat gag gcc aaa gtg aag gct ctg gag gag aag gag gag Ala Asp Glu Tyr Glu Ala Lys Val Lys Ala Leu Glu Glu Lys Glu Glu 815 820 825			2499
gag gag agg gtg gca gcc aag aaa gta ggc aca gaa att tgc aat ggc Glu Glu Arg Val Ala Ala Lys Lys Val Gly Thr Glu Ile Cys Asn Gly 830 835 840			2547
ggc cca gca ccc aag tct tca acc tgc tgt atc ctg tga gcaactggctcc Gly Pro Ala Pro Lys Ser Ser Thr Cys Cys Ile Leu			2596 845 850
cgtaggggacc ctatggctcc ctcaatcttc acccactagg atttgggttc tgcctgtggc			2656
tatttgctac aagagggttag gaagcccaag aaaatgactg aagatcattc tggatatatt			2716
aatttttttt tttttttttt ttttgagatg gagtcttgct ctgtcaccga ggctggagtg			2776
ccgtggcacg atctcagctc actgcaacct ccacctccca ggttcaagcg attctcgtgc			2836
ctcagcctcc tgagtagctg ggactacagg cgcccaccac cacacatgct aatttttgta			2896
ttttcagtac agatgggggtt tcaccatatt gggcaggctg gtctcgaact cctgacctca			2956
ggtgatcacc gcctcagctt cctgaagtgc tgggattaca ggcattgagcc accacgcccc			3016
gcctgttttt ataaactgaa gccaaactgtg aataaaactgt agcctacatt actcatccat			3076
ttttggatag ttaccactgg gagacctttg aaaagggtcc atgaactctg aaatcactga			3136
gaacatttgc agccacacat gtacatatgt gtacacaggt agacagatgg acacaggccg			3196
tttctcatcc agtttaggaa aacacacatg ctacag			3231

&lt;210&gt; 4

&lt;211&gt; 854

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 4

Met Ser Leu Ser Glu Glu Gln Ala Arg Ser Phe Leu Asp Gln Asn Pro  
1 5 10 15

Asp Phe Ala Arg Gln Tyr Phe Gly Lys Lys Leu Ser Pro Glu Asn Val  
20 25 30

Gly Arg Gly Cys Glu Asp Gly Cys Pro Pro Asp Cys Asp Ser Leu Arg  
35 40 45

Asp Leu Cys Gln Val Glu Glu Ser Thr Ala Leu Leu Glu Leu Val Gln  
50 55 60

Asp Met Gln Glu Ser Ile Asn Met Glu Arg Val Val Phe Lys Val Leu  
65 70 75 80

Arg Arg Leu Cys Thr Leu Leu Gln Ala Asp Arg Cys Ser Leu Phe Met  
85 90 95

Tyr Arg Gln Arg Asn Gly Val Ala Glu Leu Ala Thr Arg Leu Phe Ser  
100 105 110

Val Gln Pro Asp Ser Val Leu Glu Asp Cys Leu Val Pro Pro Asp Ser  
115 120 125

Glu Ile Val Phe Pro Leu Asp Ile Gly Val Val Gly His Val Ala Gln  
130 135 140

Thr Lys Lys Met Val Asn Val Glu Asp Val Ala Glu Cys Pro His Phe  
145 150 155 160

Ser Ser Phe Ala Asp Glu Leu Thr Asp Tyr Lys Thr Lys Asn Met Leu  
165 170 175

Ala Thr Pro Ile Met Asn Gly Lys Asp Val Val Ala Val Ile Met Ala  
180 185 190

Val Asn Lys Leu Asn Gly Pro Phe Phe Thr Ser Glu Asp Glu Asp Val

195                      200                      205  
 Phe Leu Lys Tyr Leu Asn Phe Ala Thr Leu Tyr Leu Lys Ile Tyr His  
   210                      215                      220  
 Leu Ser Tyr Leu His Asn Cys Glu Thr Arg Arg Gly Gln Val Leu Leu  
   225                      230                      235                      240  
 Trp Ser Ala Asn Lys Val Phe Glu Glu Leu Thr Asp Ile Glu Arg Gln  
                     245                      250                      255  
 Phe His Lys Ala Phe Tyr Thr Val Arg Ala Tyr Leu Asn Cys Glu Arg  
                     260                      265                      270  
 Tyr Ser Val Gly Leu Leu Asp Met Thr Lys Glu Lys Glu Phe Phe Asp  
                     275                      280                      285  
 Val Trp Ser Val Leu Met Gly Glu Ser Gln Pro Tyr Ser Gly Pro Arg  
                     290                      295                      300  
 Thr Pro Asp Gly Arg Glu Ile Val Phe Tyr Lys Val Ile Asp Tyr Ile  
   305                      310                      315                      320  
 Leu His Gly Lys Glu Glu Ile Lys Val Ile Pro Thr Pro Ser Ala Asp  
                     325                      330                      335  
 His Trp Ala Leu Ala Ser Gly Leu Pro Ser Tyr Val Ala Glu Ser Gly  
                     340                      345                      350  
 Phe Ile Cys Asn Ile Met Asn Ala Ser Ala Asp Glu Met Phe Lys Phe  
                     355                      360                      365  
 Gln Glu Gly Ala Leu Asp Asp Ser Gly Trp Leu Ile Lys Asn Val Leu  
   370                      375                      380  
 Ser Met Pro Ile Val Asn Lys Lys Glu Glu Ile Val Gly Val Ala Thr  
   385                      390                      395                      400  
 Phe Tyr Asn Arg Lys Asp Gly Lys Pro Phe Asp Glu Gln Asp Glu Val  
                     405                      410                      415  
 Leu Met Glu Ser Leu Thr Gln Phe Leu Gly Trp Ser Val Met Asn Thr  
                     420                      425                      430  
 Asp Thr Tyr Asp Lys Met Asn Lys Leu Glu Asn Arg Lys Asp Ile Ala  
                     435                      440                      445

Gln Asp Met Val Leu Tyr His Val Lys Cys Asp Arg Asp Glu Ile Gln  
 450 455 460

Leu Ile Leu Pro Thr Arg Ala Arg Leu Gly Lys Glu Pro Ala Asp Cys  
 465 470 475 480

Asp Glu Asp Glu Leu Gly Glu Ile Leu Lys Glu Glu Leu Pro Gly Pro  
 485 490 495

Thr Thr Phe Asp Ile Tyr Glu Phe His Phe Ser Asp Leu Glu Cys Thr  
 500 505 510

Glu Leu Asp Leu Val Lys Cys Gly Ile Gln Met Tyr Tyr Glu Leu Gly  
 515 520 525

Val Val Arg Lys Phe Gln Ile Pro Gln Glu Val Leu Val Arg Phe Leu  
 530 535 540

Phe Ser Ile Ser Lys Gly Tyr Arg Arg Ile Thr Tyr His Asn Trp Arg  
 545 550 555 560

His Gly Phe Asn Val Ala Gln Thr Met Phe Thr Leu Leu Met Thr Gly  
 565 570 575

Lys Leu Lys Ser Tyr Tyr Thr Asp Leu Glu Ala Phe Ala Met Val Thr  
 580 585 590

Ala Gly Leu Cys His Asp Ile Asp His Arg Gly Thr Asn Asn Leu Tyr  
 595 600 605

Gln Met Lys Ser Gln Asn Pro Leu Ala Lys Leu His Gly Ser Ser Ile  
 610 615 620

Leu Glu Arg His His Leu Glu Phe Gly Lys Phe Leu Leu Ser Glu Glu  
 625 630 635 640

Thr Leu Asn Ile Tyr Gln Asn Leu Asn Arg Arg Gln His Glu His Val  
 645 650 655

Ile His Leu Met Asp Ile Ala Ile Ile Ala Thr Asp Leu Ala Leu Tyr  
 660 665 670

Phe Lys Lys Arg Ala Met Phe Gln Lys Ile Val Asp Glu Ser Lys Asn  
 675 680 685

Tyr Gln Asp Lys Lys Ser Trp Val Glu Tyr Leu Ser Leu Glu Thr Thr  
 690 695 700

Arg Lys Glu Ile Val Met Ala Met Met Met Thr Ala Cys Asp Leu Ser  
705 710 715 720

Ala Ile Thr Lys Pro Trp Glu Val Gln Ser Lys Val Ala Leu Leu Val  
725 730 735

Ala Ala Glu Phe Trp Glu Gln Gly Asp Leu Glu Arg Thr Val Leu Asp  
740 745 750

Gln Gln Pro Ile Pro Met Met Asp Arg Asn Lys Ala Ala Glu Leu Pro  
755 760 765

Lys Leu Gln Val Gly Phe Ile Asp Phe Val Cys Thr Phe Val Tyr Lys  
770 775 780

Glu Phe Ser Arg Phe His Glu Glu Ile Leu Pro Met Phe Asp Arg Leu  
785 790 795 800

Gln Asn Asn Arg Lys Glu Trp Lys Ala Leu Ala Asp Glu Tyr Glu Ala  
805 810 815

Lys Val Lys Ala Leu Glu Glu Lys Glu Glu Glu Glu Arg Val Ala Ala  
820 825 830

Lys Lys Val Gly Thr Glu Ile Cys Asn Gly Gly Pro Ala Pro Lys Ser  
835 840 845

Ser Thr Cys Cys Ile Leu  
850

<210> 5

<211> 21

<212> DNA

<213> Artificial

<400> 5

gcaagctgac cctgaagttc a

21

<210> 6

<211> 19

<212> RNA

<213> Artificial

<400> 6  
gcaagcugac ccugaaguu

19

<210> 7

<211> 19

<212> RNA

<213> Artificial

<400> 7  
aacuucaggg ucagcuugc

19

<210> 8

<211> 21

<212> DNA

<213> Artificial

<400> 8  
aattctccga acgtgtcacg t

21

<210> 9

<211> 21

<212> DNA/RNA

<213> Artificial

<400> 9  
uucuccgaac gugucacgut t

21

<210> 10

<211> 21

<212> DNA/RNA

<213> Artificial

<400> 10  
acgugacacg uucggagaat t

21